SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i. APPLICANT: Hartley, James L.

    (ii) TITLE OF INVENTION: Nucleic Acid Marker Ladder For
        Estimating Mass

    (iii. NUMBER OF SEQUENCES: 12

    (iv. CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox
        (B) STREET: 1100 New York Avenue, Suite 600
        (C) CITY: Washington
        (D) STATE: D.C.
        (E) COUNTRY: USA
        (F) ZIP: 20005

    (v. COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi. CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 09/114,911
        (B) FILING DATE: 14-JUL-1998
        (C) CLASSIFICATION:

    (vii. PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/893,523
        (B) FILING DATE: 11-JUL-1997

    (vii. PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/142,124
        (B) FILING DATE: 28-OCT-1993

    (viii. ATTORNEY/AGENT INFORMATION:
        (A) NAME: McPhail, Donald R.
        (B) REGISTRATION NUMBER: 35,811
        (C) REFERENCE/DOCKET NUMBER: 0942.2570002

    (ix. TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (202) 371-2600
        (B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

    (i. SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 41 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AUCUGACCUC AUAATTTACG GAAGCATAAA GTGTAAAGCC T   41

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 38 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGUCACAGCU AUAATATTGG AAATGTGCGC GGAACCCC   38

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 41 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AUAGCUGUGA CUAATTTACT AGTGAATCCA CAGAAACTAG C   41

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 41 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACAUCUGGAC UUAATATTAG ACATATTGAT AAGGTGGCGA G   41

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 41 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGUCCAGAU GUAATTTAGG GACAGTTTGG CAAGGTTTTT A   41

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 42 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AUGAGGUCAG AUAATATTTA AGCCTTTTTG ATGTTCATCA GG   42

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 34 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: both
       (D) TOPOLOGY: both

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTCGAAGCGG CCGGTAATGA ATCGGCCAAC GCGC   34

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 26 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: both
       (D) TOPOLOGY: both

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGCGCGACG TCAGGTGGCA CTTTTC   26

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 36 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: both
       (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCGTGCGG CCGCGGTTGC TGACTAATTG AGATGC   36

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: both

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGATCCGTGA GGTGAGCCTA GGAATG   26

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 34 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: both

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGATCTGCGG CCGCGGTCTT GTCATTATCA CCGG   34

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: both

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATCGATGTTG CCCAGACTCG TTAAGC   26